Dataset S1. Predicted BqsR-regulated genes identified by regular expression and PWM

Gene	Regular expression (3A)	e-value	Function
PA14_29690	+	0.047	hypothetical
PA14_29710	+	0.047	bqsP
PA14_07060	+	0.07	Predicted phosphoesterase (cog)
PA14_07070	+	0.07	Predicted ferric reductase (cog)
PA14_04250	+	0.092	ABC-type spermidine/putrescine transport systems, ATPase components (cog, prk)
PA14_04270	+	0.092	transcription factor (PseudoCAP Function Class)
PA14_32250	+	0.18	hypothetical
PA14_32270	+	0.18	outer membrane porin, OprD family (pfam)
PA14_04180	+	0.25	Bacterial OB-Fold protein (pfam)
PA14_63110	+	0.53	S-adenosylmethionine decarboxylase (cog, pfam, tigrfam); Spermidine synthase (cog, pfam, tigrfam) operon
PA14_32580	+	0.65	Response regulator (cog, pfam, cd)
PA14_32590	+	0.65	Thiol:disulfide interchange protein (cog, prk)
PA14_35790	+	1	Homospermidine synthase (cog)
PA14_57880	+	1	ABC-type transport system involved in resistance to organic solvents, ATPase component (cog)
PA14_57890	+	1	Predicted sugar phosphate isomerase involved in capsule formation (cog)
PA14_01240	+	1.1	Zn-binding carbonic anhydrase (doi: 10.1099/mic.0.066357-0)
PA14_18370	+	1.3	UDP-4-amino-4-deoxy-L-arabinose--oxoglutarate aminotransferase (cog)
PA14_54120	+	1.9	ACP phosphodieterase (cog)
PA14_54130	+	1.9	Transcriptional regulator (cog, pfam)
PA14_58390		2.3	ABC-type dipeptide transport system, periplasmic component (cog, prk, cd)
aguB	+	3.5	N-carbamoylputrescine amidase (tigrfam, cd)
PA14_52340	+	3.5	hypothetical
PA14_52350	+	3.5	hypothetical
PA14_35300	+	3.8	Gluconate 2-dehydrogenase subunit 3 (pfam)
PA14_31630		3.8	LysR substrate binding domain (pfam, prk)
PA14_31640		3.8	This conserved domain belongs to a superfamily including the bleomycin (cd) resistance protein, glyoxalase I, and type I ring-cleaving dioxygenases
oprH		3.8	outer membrane porin stabilizes outer membrane by LPS binding and increases antibiotic resistance (doi: 10.1074/jbc.M111.280933)
napE	+	3.8	nitrate reductase periplasmic (PMID: 9560320)
PA14_24350	+	4.4	cprR - phosphorelay response regulator activity antimicrobial peptide activated(PMID: 23006746)

PA14_24360	+	4.4	Peptidase S8 family domain in Autotransporter serine proteases (cd)
PA14_46900	+	4.5	hypothetical
PA14_46910	+	4.5	ABC-type amino acid transport/signal transduction systems, periplasmic component/domain (cog)
PA14_37990	+	8.2	RNA polymerase sigma factor (cog, prk,tigrfam)
PA14_38000	+	8.2	hypothetical
algD	+	8.2	GDP-mannose 6-dehydrogenase AlgD (PMID: 12705829, PMID: 7521247)
PA14_61840	+	8.6	Plasmid maintenance system antidote protein (cog)
PA14_61850	+	8.6	Outer membrane receptor proteins, mostly Fe transport (cog)
lasR	+	10	quorum sensing transcription factor
PA14_34150	+	12	Transcriptional regulators containing an AAA-type ATPase domain and a DNA-binding domain (cog)
PA14_02520		14	hypothetical
PA14_02530		14	Predicted esterase of the alpha/beta hydrolase fold (cog)
PA14_24690	+	16	D-alanyl-D-alanine carboxypeptidase (penicillin-binding protein 4) (cog)
PA14_24700		16	hypothetical
PA14_40170		19	Membrane transporters of cations and cationic drugs (cog)
PA14_40180		19	Aerobic-type carbon monoxide dehydrogenase, small subunit CoxS/CutS homologs (cog)
feoA	+	23	Fe2+ transport system protein A
PA14_63470		25	S-adenosylmethionine-dependent methyltransferases (CD), Methyltransferase domain (pfam)
PA14_02760		25	cyl CoA:acetate/3-ketoacid CoA transferase, alpha subunit (cog)
PA14_47380		27	TonB-dependent heme/hemoglobin receptor family protein (tigrfam)
PA14_54830		29	Predicted hydrolases or acyltransferases (cog)
PA14_27070		32	Predicted membrane protein (cog)
PA14_21020	+	32	Non-ribosomal peptide synthetase modules and related proteins (cog)
PA14_21030	+	32	ATP-dependent Clp protease proteolytic subunit (prk, cog)
metN		32	DL-methionine transporter ATP-binding subunit (prk)
PA14_38380	+	35	Transcriptional regulator (cog)
PA14_38395	+	35	periplasmic multidrug efflux lipoprotein precursor (prk)
PA14_08600		35	23S ribosomal RNA
PA14_55631		35	23S ribosomal RNA
PA14_62060		35	23S ribosomal RNA
PA14_70880		35	23S ribosomal RNA
PA14_07430	+	36	hypothetical
PA14_17380		38	LysR family transcriptional regulator (prk)
adhC		38	Zn-dependent alcohol dehydrogenases, class III(cog)
PA14_44820		38	Transthyretin-like protein (cog)
PA14_44830		38	Catalytic domain of bacterial PuuE allantoinases, Schizosaccharomyces pombe chitin deacetylase 1 (SpCDA1), and similar proteins (cd)

PA14_58375	+	43	Xaa-Pro aminopeptidase (cog)
PA14_58380	+	43	Predicted transcriptional regulators (cog)
PA14_59550		43	hypothetical
PA14_52960		43	hypothetical
PA14_10080		45	hypothetical
PA14_10090		45	Transcriptional regulator (cog)
PA14_01490		45	hemolysin
PA14_25840		47	Dehydrogenases (flavoproteins) [Energy production and conversion] (cog)
etfB		47	Electron transfer flavoprotein, beta subunit (cog)
PA14_55380		47	Hemolysin activation/secretion protein (cog)
PA14_63220	+		hypothetical
PA14_35740	+		Transposase and inactivated derivatives, TnpA family (cog)
mexG	+		hypothetical part of operon MexGHI-OpmD efflux pump confers resistence to vanadium and is probably involved in acyl-homoserine lactone homeostasis. (cog)
PA14_51610	+		hypothetical
PA14_51620	+		Transposase and inactivated derivatives (cog)
PA14_51310	+		Predicted redox protein, regulator of disulfide bond formation (cog)
PA14_51320	+		Putative Zn-dependent protease, contains TPR repeats [General function prediction only] (cog)
PA14_13890	+		Integrase core domain (pfam)
PA14_35210	+		Transcriptional regulator [Transcription] (cog)
PA14_35230	+		Sugar phosphate permease (cog)
PA14_31130	+		hypothetical
PA14_28200	+		hypothetical
PA14_31350	+		Uncharacterized NAD(FAD)-dependent dehydrogenases [General function prediction only] (cog)
PA14_56790	+		Predicted signal transduction protein containing a membrane domain, an EAL and a GGDEF domain (cog)
PA14_14160	+		Xenobiotic acyltransferase (XAT): The XAT class of hexapeptide acyltransferases is composed of a large number of microbial enzymes that catalyze the CoA-dependent acetylation of a variety of hydroxyl-bearing acceptors such as chloramphenicol and streptogramin, among others (CD)
aprA	+		alkaline metalloproteinase (pdb 1XAP, 1AKL)
PA14_32710	+		RNA polymerase sigma factor (cog, prk,tigrfam, pfam)
PA14_18870	+		hypothetical